

GenCore version 4.5
Copyright (c) 1993 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2002, 17:24:09, Search time 37.13 Seconds

(without alignments)

29,387 Million cell updates/sec

Title: us-09-786-009-6

Perfect score: 166

Sequence: 1 CAYKTCANKHLLVACEGNYVHPDASY 30

oring table: BLOSUM62

Gap0 10.0, Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 6

Maximum fw seq length: 20000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SWISSProt_39:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	166	100.0	150	1	P00656 Bos taurus
2	163	92.2	124	1	RNF_RUBIN
3	160	96.4	124	1	RNF_AEHE
4	159	96.4	124	1	RNF_CACTE
5	157	94.6	124	1	RNF_SHEEP
6	157	94.6	124	1	RNF_ANTAM
7	156	94.0	124	1	RNF_AUCOA
8	156	94.0	124	1	RNF_CAPPA
9	156	94.0	124	1	RNF_PANTA
10	155	93.4	124	1	RNF_CONTA
11	154	92.9	124	1	RNF_CANKO
12	153	92.2	124	1	RNF_CLECA
13	152	91.6	124	1	RNF_PAPAP
14	151	91.0	124	1	RNF_CEPER
15	151	91.0	124	1	RNF_DAMPA
16	147	89.6	124	1	RNF_AXIFA
17	146	88.6	124	1	RNF_BOSTR
18	145	87.2	124	1	RNF_BALAC
19	145	87.3	149	1	RNF_MOUSE
20	144	86.7	128	1	RNF_MOUSE
21	143	86.1	124	1	RNF_HIVAM
22	141	84.9	149	1	RNF_PAPAP
23	140	84.3	124	1	RNF_CAMP
24	139	83.7	125	1	RNF_CVHEH
25	139	83.7	128	1	RNF_CHOHO
26	139	83.7	148	1	RNF_CPRNT
27	137	82.5	124	1	RNF_CUBIK
28	136	81.9	124	1	RNF_PIG
29	136	81.9	141	1	RNF_CIPCA
30	136	81.9	151	1	RNF_AXIPE
31	136	81.9	152	1	RNF_FAT
32	135	81.3	128	1	RNF_PVOCG
33	135	81.3	148	1	RNF_MICNV

34	135	81.3	151	1	RNF_CIPCA	P74351 caprine
35	134	80.7	128	1	RNF_HOCHB	P06277 hydroxy
36	134	80.7	128	1	RNF_PIG	P04059 porcine
37	134	80.7	150	1	RNF_PIG	P09559 porcine
38	134	80.7	150	1	RNF_HOCHB	P04398 human
39	133	80.1	150	1	RNF_CIPCA	P04372 porcine
40	133	80.1	149	1	RNF_SHEEP	P09543 ovine
41	133	80.1	149	1	RNF_HOCHB	P09545 porcine
42	133	80.1	149	1	RNF_PIG	P09542 porcine
43	133	80.1	167	1	RNF_PIG	P09573 porcine
44	131	78.9	148	1	RNF_PIG	P09574 porcine
45	131	78.9	149	1	RNF_PIG	P09575 porcine

ALIGNMENT

RESULT	ID	SEQUENCE	STANDARD	PRT	AA
1	RNF_MOUSE				
AC	P00656				
BT	21-JUL-1986 (rel. 01, created)				
BT	01-NOV-1988 (rel. 09, last sequence update)				
BT	20-AUG-2001 (rel. 40, last annotation update)				
DE	RIBONUCLEASE PANCREATIC PRECURSOR (EC 3.1.27.5) (RNASE 1) (RNASE A)				
EN	RNASE1 OR PNS1				
OS	Bos taurus (Bovine), and Bison bison (American bison).				
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Artiodactyla; Bovidae; Bovidae;				
OX	NCBI_TaxID:9913, 9901;				
RN	[1]				
RP	SEQUENCE FROM N.A				
RC	SPECIES: bovine				
RX	MEDLINE: 84262572 PubMed 235818;				
EX	Carlsana A., Contarone E., Palmetti M., Lombardi M., Far A.;				
RT	Structure of the bovine pancreatic ribonuclease gene: the unique				
RT	intervening sequence in the 5' untranslated region contains a				
RT	promoter-like element."				
RL	Nucleic Acids Res. 16:5491-5492(1988)				
RN	[2]				
RP	SEQUENCE OF 27 JEN FROM N.A.				
RC	SPECIES: bovine				
EX	MEDLINE: 94592920 PubMed 215688;				
EX	Delacourte S.B., Ritz M., Viret M., Viret M., Ruller W.F.;				
RA	Reines R.T.;				
RT	Engineering ribonuclease A production and secretion in				
RT	characterization of wild-type enzymes and mutant strains.				
RT	Protein Eng. 8:26-27(1995).				
RL	[3]				
RP	SEQUENCE OF 27 JEN, AM. FROM GEN. 10065				
RC	SPECIES: bovine				
PA	Smith R.C. (1970) W.B. 96: 96-100				
RT	"The sequence of amino acid residues in bovine pancreatic				
RT	ribonuclease: new findings and confirmations."				
FL	J. Biol. Chem. 245:227-234(1963).				
FP	[4]				
RP	SEQUENCE OF 27-150.				
RC	SPECIES: bovine				
BA	Plummer T.M., Jr., Hirs C.H.W.				
BT	On the structure of bovine pancreatic ribonuclease: Isolation of				
BT	a 917-residue fragment."				
BT	J. Biol. Chem. 240:270-278(1964)				
EN	[5]				
RP	ACTIVE SITE.				
RC	SPECIES: bovine				
BA	Reichman R.L., Smith R.H., Hirs C.H.W.				
BT	The reactivities of the histidine residues in the active site of				
BT	ribonuclease: localization of the active site and the effect of				
BT	J. Biol. Chem. 240:2921-2928(1965)				
RN	[6]				
RP	ACTIVE SITE.				
RC	SPECIES: bovine				

RX MEDLINE 69260124; PubMed 5801478;
 RA Stahl S., Barford D.A.;
 RP "Heavy atom labelling and refinement of bovine pancreatic ribonuclease
 R1 structure: locations of ribonuclease with N-acetylmethylcysteine
 R2 (hydroxy and sulfur bond)."
 R3 J. Mol. Biol. 411:247-254(1999).
 R4 171
 R5 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 R6 SPECIES: BOVINE.
 R7 MEDLINE 7002245; PubMed 5400097;
 R8 Wyckoff H.W., Isenrodt D., Hanson A.W., Knox J.R., Lee B.,
 R9 Richards F.M.;
 R10 "The three-dimensional structure of ribonuclease-S. Interpretation of
 R1 an electron density map at a nominal resolution of 2 A."
 R2 J. Biol. Chem. 245:405-428(1970).
 R3 181
 R4 X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 R5 SPECIES: BOVINE.
 R6 MEDLINE 74283424; PubMed 4857267;
 R7 Carlisle C.J., Palmer R.A., Mozumdar S.K., Gouletsky B.A.;
 R8 "The structure of ribonuclease at 2.5 A resolution."
 R9 J. Mol. Biol. 85:118(1974).
 R10 191
 R11 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 R12 SPECIES: BOVINE.
 R13 MEDLINE 82120062; PubMed 6276480;
 R14 Wlodawer A., Bort R., Shottlin L.;
 R15 "The refined crystal structure of ribonuclease A at 2.0-A
 R6 resolution."
 R7 J. Biol. Chem. 267:1145-1142(1982).
 R8 1101
 R9 X-RAY CRYSTALLOGRAPHY (1.26 ANGSTROMS).
 R10 SPECIES: BOVINE.
 R11 MEDLINE 8824009; PubMed 4401445;
 R12 Wlodawer A., Szymanski L.A., Shottlin L., Gilliland G.L.;
 R13 "Structure of phosphatidyl-ribonuclease A refined at 1.26 A."
 R14 Biochemistry 27:2705-2717(1988).
 R15 1111
 R16 X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
 R17 MEDLINE 9229793; PubMed 9154942;
 R18 Lounibos D.P., Shapiro R., Treas L., Russo N., Arhatya K.R.;
 R19 "Crystal structures of ribonuclease A complexes with 5'
 R20 diphosphonates: 4' phosphate and 5' diphosphonates."
 R21 Biochemistry 36:5568-5588(1997).
 R22 1121
 R23 STRUCTURE BY NMR.
 R24 SPECIES: BOVINE.
 R25 MEDLINE 8937545; PubMed 2775743;
 R26 Robertson A.D., Partisano E.O., Eastman M.A., Scheraga H.A.;
 R27 "Proton NMR assignment and regular backbone structure of bovine
 R28 pancreatic ribonuclease A in aqueous solution."
 R29 Biochemistry 28:5940-5948(1989).
 R30 1131
 R31 STRUCTURE BY NMR.
 R32 SPECIES: BOVINE.
 R33 MEDLINE 8937850; PubMed 2776767;
 R34 Eves M., Brink M., Santoro J., Gonzalez C., Neira J.L., Nieto J.L.,
 R35 Bortan J.;
 R36 "Sequential 1H-NMR assignment and solution structure of bovine
 R37 pancreatic ribonuclease A."
 R38 J. Biomol. NMR 18:623-638(1988).
 R39 1141
 R40 STRUCTURE BY NMR.
 R41 SPECIES: BOVINE.
 R42 MEDLINE 9404599; PubMed 1441699;
 R43 Riva M., Santoro J., Gonzalez C., Brink M., Neira J.L., Nieto J.L.,
 R44 Bortan J.;
 R45 "3D structure of bovine pancreatic ribonuclease A in aqueous
 R46 solution: an approach to tertiary structure determination from a
 R47 small basis of 1H NMR NOE correlations."
 R48 J. Biomol. NMR 1:283-298(1991).

RN [15]
 RP DNA-BINDING.
 R1 SPECIES: BOVINE.
 R2 MEDLINE 86179400; PubMed 3961503;
 R3 McPherson A., Brayer G., Casco D., Williams R.;
 R4 "The mechanism of binding of a polynucleotide chain to pancreatic
 R5 ribonuclease."
 R6 Science 232:765-768(1986).
 R7 1161
 R8 SEQUENCE OF 27-150.
 R9 SPECIES: B. BOVINE.
 R10 MEDLINE 76259366; PubMed 955781;
 R11 Muskiet F.A.J., Mellini G.W., Peintema J.J.;
 R12 "Studies on the primary structure of bovine pancreatic ribonuclease."
 R13 Int. J. Pept. Protein Res. 8:345-348(1976).
 R14 1- CATALYTIC ACTIVITY: ENDOPEPTIDOLYTIC CLEAVAGE TO 3'-PHOSPHOMONO-
 R15 NUCLEOTIDES AND 3'-PHOSPHOOLIGONUCLEOTIDES ENDING IN C-P OR U-P
 R16 WITH 2',3'-CYCLIC PHOSPHATE INTERMEDIATES.
 R17 1- SUBCELLULAR LOCATION: SECRETED.
 R18 1- MISCELLANEOUS: RIBONUCLEASE CAN DESTABILIZE OR BIND THE RNA
 R19 HELIX BY COMPLEXING WITH SINGLE-STRANDED RNA. THIS COMPLEX ARISES
 R20 BY AN EXTENDED MULTISITE CATION-ANION INTERACTION BETWEEN THE
 R21 LYSINE AND ARGININE RESIDUES OF THE ENZYME AND THE PHOSPHATE
 R22 GROUPS OF THE NUCLEOTIDES.
 R23 1- MISCELLANEOUS: THE R158R SEQUENCE APPEARS TO BE IDENTICAL WITH
 R24 THAT OF BOVINE.
 R25 1- SIMILARITY: REFERENCES TO THE PANCREATIC RIBONUCLEASE FAMILY.
 R26 1- DATABASE: NAME CONTRIBUTION TO THE ENZYME MANUAL;
 R27 WWW="http://www.worthington-biochem.com/eng/engname.html".
 R28 1- THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 R29 between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 R30 the European Bioinformatics Institute. There are no restrictions on its
 R31 use by non-profit institutions as long as its content is in no way
 R32 modified and this statement is not removed. Usage by and for commercial
 R33 entities requires a license agreement (see <http://www.ebi.ac.uk/infocentre/>
 R34 or send an email to license@ebi.ac.uk).
 R35 1- EMBL: X07283; CAA30263.1;
 R36 EMBL: S80747; AAB45594.1;
 R37 PIR: A00804; NRBO.
 R38 PIR: A91771; NRBO.
 R39 PIR: A32471; A32471.
 R40 PIR: S00897; S00897.
 R41 PIR: S05528; S05528.
 R42 PDB: 1RBA; 15-JUL-92.
 R43 PDB: 1RBA; 15-OCT-91.
 R44 PDB: 1RBA; 15-OCT-91.
 R45 PDB: 1RBA; 15-OCT-89.
 R46 PDB: 1SRN; 15-JUL-92.
 R47 PDB: 5RSA; 15-APR-93.
 R48 PDB: 6RSA; 15-OCT-89.
 R49 PDB: 7RSA; 15-JAN-93.
 R50 PDB: 8RSA; 15-APR-91.
 R51 PDB: 9RSA; 15-APR-91.
 R52 PDB: 1RAT; 15-JUL-93.
 R53 PDB: 1RAT; 15-JUL-93.
 R54 PDB: 3RAT; 15-JUL-93.
 R55 PDB: 4RAT; 15-JUL-93.
 R56 PDB: 5RAT; 15-JUL-93.
 R57 PDB: 6RAT; 15-JUL-93.
 R58 PDB: 7RAT; 15-JUL-93.
 R59 PDB: 8RAT; 15-JUL-93.
 R60 PDB: 9RAT; 15-JUL-93.
 R61 PDB: 1RBA; 15-OCT-93.
 R62 PDB: 1RBA; 15-OCT-93.
 R63 PDB: 1RBA; 15-OCT-93.
 R64 PDB: 1RBA; 15-OCT-93.
 R65 PDB: 1RBA; 15-OCT-93.
 R66 PDB: 1RBA; 15-OCT-93.
 R67 PDB: 1RBA; 15-OCT-93.
 R68 PDB: 1RBA; 15-OCT-93.
 R69 PDB: 1RBA; 15-OCT-93.
 R70 PDB: 1RBA; 15-OCT-93.
 R71 PDB: 1RBA; 15-OCT-93.
 R72 PDB: 1RBA; 15-OCT-93.
 R73 PDB: 1RBA; 15-OCT-93.
 R74 PDB: 1RBA; 15-OCT-93.
 R75 PDB: 1RBA; 15-OCT-93.
 R76 PDB: 1RBA; 15-OCT-93.
 R77 PDB: 1RBA; 15-OCT-93.
 R78 PDB: 1RBA; 15-OCT-93.
 R79 PDB: 1RBA; 15-OCT-93.
 R80 PDB: 1RBA; 15-OCT-93.
 R81 PDB: 1RBA; 15-OCT-93.
 R82 PDB: 1RBA; 15-OCT-93.
 R83 PDB: 1RBA; 15-OCT-93.
 R84 PDB: 1RBA; 15-OCT-93.
 R85 PDB: 1RBA; 15-OCT-93.
 R86 PDB: 1RBA; 15-OCT-93.
 R87 PDB: 1RBA; 15-OCT-93.
 R88 PDB: 1RBA; 15-OCT-93.
 R89 PDB: 1RBA; 15-OCT-93.
 R90 PDB: 1RBA; 15-OCT-93.
 R91 PDB: 1RBA; 15-OCT-93.
 R92 PDB: 1RBA; 15-OCT-93.
 R93 PDB: 1RBA; 15-OCT-93.
 R94 PDB: 1RBA; 15-OCT-93.
 R95 PDB: 1RBA; 15-OCT-93.
 R96 PDB: 1RBA; 15-OCT-93.
 R97 PDB: 1RBA; 15-OCT-93.
 R98 PDB: 1RBA; 15-OCT-93.
 R99 PDB: 1RBA; 15-OCT-93.
 R100 PDB: 1RBA; 15-OCT-93.

GN RNASEL OR RNSE.
GN Antilocapra americana (Pronhorn).
GC Eukaryota: Metazoa: Chordata: Cnidaria: Vertebrata: Euteleostomi.
GC Mammalia: Perissodactyla: Equitipodidae: Equulini: Equus. Revidata.
GC Antilocapridae: Antilocapra.
GC NCBI_Taxid:9851;
KN [1]
RP SPOURNE.
RC TISSUE: Pancreas;
RX MEDLINE: 80075014; PubMed:51311;
RA Reintema 11. "Asastra W. Muntjema 1.
RA "Primary structure of pronhorn pancreatic ribonuclease: close
RA relationship between albatre and pronhorn."
RA J. Mol. Evol. 13:305-316(1979).
CC -1- CATALYTIC ACTIVITY: ENDONUCLEOTIC CLEAVAGE TO 3'-PHOSPHOMONO-
CC NUCLEOTIDES AND 5'-PHOSPHOSULFONICACID ENDINGS IN C P OR U-P
CC WITH 2,3'-CYCLIC PHOSPHATE INTERMEDIATES.
CC -1- SUBCELLULAR LOCATION: PANCREAS.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC PR: APOB12; NPREL.
DR HSSE: P00056; 1880.
DR InterPro: IPR001427; RNASEA.
DR Pfam: PF00074; RNASEA_1.
DR PRINTS: PP00794; RHNDEUTENE.
DR ProDom: PD000935; RNASEA_1.
DR SMART: SM00092; RNASEA_P01.
DR PROSITE: PS00127; RNASE_PANCREATIC_1.
KW hydrolyase; Nucleoside; Endonuclease; Cysteine-rich.
FT DIISLEPID 26 84
FT DIISLEPID 40 95
FT DIISLEPID 58 110
FT DIISLEPID 65 72
FT ACT_SITE 12 42
FT ACT_SITE 41 41
FT ACT_SITE 119 119
FT CARBOHYD 34 34
FT SPOURNE 124 AA; 1371 MW; 94355551420852 PROCE4;
GCRTY MATCH. 94.5% SCORE 157 CR 1 GATH 124.
Host Local Similarity 93.3% Prod. No. 2.4e-16;
Matches 297 Corrected for 1 Mismatches 1; Indels 0; Gaps 0
QY 1 GAVTQANKHIVANQGVVYVHNVASV 30
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII
B 95 GAVTTEAATATATTAATGVVYVHNVASV 124
RESULT 7
ID RNF_ALCAA STANDARD; PRT; 124 AA.
AC RNF_ALCAA
AC P00667;
DI 21-JUN-1986 (Ref. 01. Created)
DI 21-JUN-1986 (Ref. 05. Last sequence update)
DI 01-NOV-1997 (Ref. 05. Last annotation update)
DE RIBONUCLEASE PANCHEATIN (EC 3.1.27.5) (RNASE P) (RNASE A).
GN RNASEL OR RNSE.
OS Alces alces alces (European moose) (ELK).
OC Eukaryota: Metazoa: Chordata: Cnidaria: Vertebrata: Euteleostomi;
OC Mammalia: Artiodactyla: Cetartiodactyla: Cervinidae: Cervidae;
OC Cervidae: Odocoileidae: Alces.
OX NCBI_Taxid:9853;
OX [1]
RP PARTIAL SPOURNE.
RC TISSUE: Pancreas;
RX MEDLINE: 74092015; PubMed:1157925.
RA Leiferlar Van den Berg G., Holmstrom J.L.;
RA "The amino acid sequences of reindeer, moose and fallow deer
RA pancreatic ribonucleases."
RA FEBS Lett. 56:101-107(1975).
CC -1- CATALYTIC ACTIVITY: ENDONUCLEOTIC CLEAVAGE TO 3'-PHOSPHOMONO-
CC NUCLEOTIDES AND 5'-PHOSPHOSULFONICACID ENDINGS IN C P OR U-P

[illegible]

```

07 1 TISSUE SPECIFICITY: PANCREAS.
08 1 SIMILARITY: MEMBERS TO THE PANCREATIC RIBONUCLEASE FAMILY.
09
10 THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
11 between the Swiss Institute of Bioinformatics and the EMBL outstation
12 at the European Bioinformatics Institute. There are no restrictions on its
13 use by non-profit institutions, as long as its content is in no way
14 modified and this statement is not removed, altered, falsified or
15 omitted in any form or by any means (electronic or mechanical), including
16 photocopying, recording, or by any information storage and retrieval system.
17
18 PDB: 1A00 (1.0)
19 PDB: 1A00 (1.0)
20 PDB: 1A00 (1.0)
21 PDB: 1A00 (1.0)
22 PDB: 1A00 (1.0)
23 PDB: 1A00 (1.0)
24 PDB: 1A00 (1.0)
25 PDB: 1A00 (1.0)
26 PDB: 1A00 (1.0)
27 PDB: 1A00 (1.0)
28 PDB: 1A00 (1.0)
29 PDB: 1A00 (1.0)
30 PDB: 1A00 (1.0)
31 PDB: 1A00 (1.0)
32 PDB: 1A00 (1.0)
33 PDB: 1A00 (1.0)
34 PDB: 1A00 (1.0)
35 PDB: 1A00 (1.0)
36 PDB: 1A00 (1.0)
37 PDB: 1A00 (1.0)
38 PDB: 1A00 (1.0)
39 PDB: 1A00 (1.0)
40 PDB: 1A00 (1.0)
41 PDB: 1A00 (1.0)
42 PDB: 1A00 (1.0)
43 PDB: 1A00 (1.0)
44 PDB: 1A00 (1.0)
45 PDB: 1A00 (1.0)
46 PDB: 1A00 (1.0)
47 PDB: 1A00 (1.0)
48 PDB: 1A00 (1.0)
49 PDB: 1A00 (1.0)
50 PDB: 1A00 (1.0)
51 PDB: 1A00 (1.0)
52 PDB: 1A00 (1.0)
53 PDB: 1A00 (1.0)
54 PDB: 1A00 (1.0)
55 PDB: 1A00 (1.0)
56 PDB: 1A00 (1.0)
57 PDB: 1A00 (1.0)
58 PDB: 1A00 (1.0)
59 PDB: 1A00 (1.0)
60 PDB: 1A00 (1.0)
61 PDB: 1A00 (1.0)
62 PDB: 1A00 (1.0)
63 PDB: 1A00 (1.0)
64 PDB: 1A00 (1.0)
65 PDB: 1A00 (1.0)
66 PDB: 1A00 (1.0)
67 PDB: 1A00 (1.0)
68 PDB: 1A00 (1.0)
69 PDB: 1A00 (1.0)
70 PDB: 1A00 (1.0)
71 PDB: 1A00 (1.0)
72 PDB: 1A00 (1.0)
73 PDB: 1A00 (1.0)
74 PDB: 1A00 (1.0)
75 PDB: 1A00 (1.0)
76 PDB: 1A00 (1.0)
77 PDB: 1A00 (1.0)
78 PDB: 1A00 (1.0)
79 PDB: 1A00 (1.0)
80 PDB: 1A00 (1.0)
81 PDB: 1A00 (1.0)
82 PDB: 1A00 (1.0)
83 PDB: 1A00 (1.0)
84 PDB: 1A00 (1.0)
85 PDB: 1A00 (1.0)
86 PDB: 1A00 (1.0)
87 PDB: 1A00 (1.0)
88 PDB: 1A00 (1.0)
89 PDB: 1A00 (1.0)
90 PDB: 1A00 (1.0)
91 PDB: 1A00 (1.0)
92 PDB: 1A00 (1.0)
93 PDB: 1A00 (1.0)
94 PDB: 1A00 (1.0)
95 PDB: 1A00 (1.0)
96 PDB: 1A00 (1.0)
97 PDB: 1A00 (1.0)
98 PDB: 1A00 (1.0)
99 PDB: 1A00 (1.0)
100 PDB: 1A00 (1.0)

```

```

07 1 TISSUE SPECIFICITY: PANCREAS.
08 1 SIMILARITY: MEMBERS TO THE PANCREATIC RIBONUCLEASE FAMILY.
09
10 THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
11 between the Swiss Institute of Bioinformatics and the EMBL outstation
12 at the European Bioinformatics Institute. There are no restrictions on its
13 use by non-profit institutions, as long as its content is in no way
14 modified and this statement is not removed, altered, falsified or
15 omitted in any form or by any means (electronic or mechanical), including
16 photocopying, recording, or by any information storage and retrieval system.
17
18 PDB: 1A00 (1.0)
19 PDB: 1A00 (1.0)
20 PDB: 1A00 (1.0)
21 PDB: 1A00 (1.0)
22 PDB: 1A00 (1.0)
23 PDB: 1A00 (1.0)
24 PDB: 1A00 (1.0)
25 PDB: 1A00 (1.0)
26 PDB: 1A00 (1.0)
27 PDB: 1A00 (1.0)
28 PDB: 1A00 (1.0)
29 PDB: 1A00 (1.0)
30 PDB: 1A00 (1.0)
31 PDB: 1A00 (1.0)
32 PDB: 1A00 (1.0)
33 PDB: 1A00 (1.0)
34 PDB: 1A00 (1.0)
35 PDB: 1A00 (1.0)
36 PDB: 1A00 (1.0)
37 PDB: 1A00 (1.0)
38 PDB: 1A00 (1.0)
39 PDB: 1A00 (1.0)
40 PDB: 1A00 (1.0)
41 PDB: 1A00 (1.0)
42 PDB: 1A00 (1.0)
43 PDB: 1A00 (1.0)
44 PDB: 1A00 (1.0)
45 PDB: 1A00 (1.0)
46 PDB: 1A00 (1.0)
47 PDB: 1A00 (1.0)
48 PDB: 1A00 (1.0)
49 PDB: 1A00 (1.0)
50 PDB: 1A00 (1.0)
51 PDB: 1A00 (1.0)
52 PDB: 1A00 (1.0)
53 PDB: 1A00 (1.0)
54 PDB: 1A00 (1.0)
55 PDB: 1A00 (1.0)
56 PDB: 1A00 (1.0)
57 PDB: 1A00 (1.0)
58 PDB: 1A00 (1.0)
59 PDB: 1A00 (1.0)
60 PDB: 1A00 (1.0)
61 PDB: 1A00 (1.0)
62 PDB: 1A00 (1.0)
63 PDB: 1A00 (1.0)
64 PDB: 1A00 (1.0)
65 PDB: 1A00 (1.0)
66 PDB: 1A00 (1.0)
67 PDB: 1A00 (1.0)
68 PDB: 1A00 (1.0)
69 PDB: 1A00 (1.0)
70 PDB: 1A00 (1.0)
71 PDB: 1A00 (1.0)
72 PDB: 1A00 (1.0)
73 PDB: 1A00 (1.0)
74 PDB: 1A00 (1.0)
75 PDB: 1A00 (1.0)
76 PDB: 1A00 (1.0)
77 PDB: 1A00 (1.0)
78 PDB: 1A00 (1.0)
79 PDB: 1A00 (1.0)
80 PDB: 1A00 (1.0)
81 PDB: 1A00 (1.0)
82 PDB: 1A00 (1.0)
83 PDB: 1A00 (1.0)
84 PDB: 1A00 (1.0)
85 PDB: 1A00 (1.0)
86 PDB: 1A00 (1.0)
87 PDB: 1A00 (1.0)
88 PDB: 1A00 (1.0)
89 PDB: 1A00 (1.0)
90 PDB: 1A00 (1.0)
91 PDB: 1A00 (1.0)
92 PDB: 1A00 (1.0)
93 PDB: 1A00 (1.0)
94 PDB: 1A00 (1.0)
95 PDB: 1A00 (1.0)
96 PDB: 1A00 (1.0)
97 PDB: 1A00 (1.0)
98 PDB: 1A00 (1.0)
99 PDB: 1A00 (1.0)
100 PDB: 1A00 (1.0)

```

	Matches	28	Conservation	0	Mismatches	2	Indels	0	Gaps	0
QY	1	CAKRTIQANKELLVAC	EGNPPVPHFASV	40						
Id	95	CAKFAIVACELLVAC	EGNPPVPHFASV	124						

Search completed: March 14, 2002, 17:45:02
 Job time: 653 sec

